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Host jumps, the acquisition by a parasite of the capacity to infect novel host species, are frequent among plant viruses but still poorly understood. To investigate their mechanisms, we performed an experimental evolution of endive necrotic mosaic virus (ENMV) in five species of the family Asteraceae, including vegetable and ornamental crops, and analysed the incurred genetic changes.

ENMV is mostly confined to wild salsify (*Tragopogon pratensis*) and occasionally infects lettuce (*Lactuca sativa*). An ENMV isolate from *L. sativa* was serially passaged in one of five plant species (either *L. sativa*, *T. pratensis*, *Calendula arvensis*, *Zinnia elegans* or *Cichorium endivia*). For each species, six infection cycles were performed, with eight independent experimental replicas. Each of the evolved ENMV populations and the initial isolate were inoculated to the five plant species to measure their pathogenicity.

Changes (gains) in virus pathogenicity were observed in *C. arvensis* and *Z. elegans* only. Cross-adaptations between *C. arvensis* and *Z. elegans* were also observed. Parallel nonsynonymous substitutions (identical substitutions arising independently) were observed at three nucleotide positions in the VPg cistron of the adapted ENMV populations, and are candidates for the observed pathogenicity changes. Some of these were shared between *C. arvensis*- and *Z. elegans*-evolved populations, partly explaining the cross-adaptations.

These results indicate that ENMV is prone to jumping to novel host species, that cross-adaptations occur and may be linked to the genetic distance between host species and that these jumps may involve the VPg in a way similar to the breakdown of eIF4E-mediated resistance.